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Result
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Maximum DB
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   3412
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seq length: 2000000000
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1: /SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp/AA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqp/AA1984.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqp/AA1987.DAT:*

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10: /SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT:*

12: /SIDS1/gcgdata/geneseq/geneseqp/AA1991.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseqp/AA1993.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseqp/AA1994.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseqp/AA1994.DAT:*

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17: /SIDS1/gcgdata/geneseq/geneseqp/AA1995.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseqp/AA1995.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseqp/AA1995.DAT:*

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20: /SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Macadamia integrif
Macadamia integrif
Sequence encoded b
Gossypium hirsutum
Theobroma cacao an Zea mays antlimicro
Hordeum vulgare an Peanut allergen Ar Arachis hypogaea a Peanut allergen, A Peanut allergen 11
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LexA/NuMA fusion p	21	18	2192	4.1	146.5	5
protein	Y55932	20	1297	4.1	146.5	44
ythn m	Y22206	20	361	4.1	146.5	43
GEK 2	Y55939	20	912	4.2	147	42
Human ZC3 protein.	Y55933	20	1326	4.4	154.5	41
l length human	Y55966	20	968	4.4	157	40
Oat globin A2B. A	R47128	15	515	4.5	159.5	39
Protein regulating	Y58633	21	1299	4.5	160	38
Human CDC28-#3 RNA	W30613	20	1041	4.6	161	37
Amino acid sequenc	Y68784	21	1135	4.6	163	36
	Y55954	20	1233	4.6	163.5	ဌ
LSA-	R26941	13	316	4.7	σ	34
iparum LSA	R26944	13	493	4.7	166	S
Ara h 3 allergen s	Y40912	20	512	4.8	169	32
ut aller	Y15246	20	510	4.8	170	31
Rice storage prote	P82755	9	499	4.8	171	30
ied oat glob	R47127	15	472	4.9	173	29
follicle st	W03627	17	360		183	28
Human ZCl protein.	Y55931	20	1239		183.5	27
Human thyrotropin	W03626	17	412		184	26
Leucocytozoan prot	R70491	16	562		ထ	25
HHV8 ORF 73 protei	Y58500	21	1.162	6.2	218.5	24
	Y30795	20	1898		226	23
T. gondii immunoqe	Y29039	20	611	6.7	237	22
haseolin A chain	Y40914	20	371	5	w	21
G. max truncated S	W90342	20	409	9.	689.5	20
ra h 1 allergen	Y40913	20	415	0.	N	19
. max trunc	W90340	20	4	0.	739	18
. max SBP2	W90341	20	8	2.	797.5	17
. max s	9033	20	524	2.	798	16
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e max anti	62	19		24.2	855.5	14
Peanut allergen Ar	21	18	626	4	5	13

## ALIGNMENTS

RESULT W62829 PR XX WPI; 1998-377279/32. N-PSDB; V42311. Bower NI, Protein кеу 20-DEC-1996; 22-DEC-1997; 02-JUL-1998. W09827805-A1. Peptide Macadamia integrifolia. antimicrobial protein; infestation; control Macadamia integrifolia antimicrobial protein 27-OCT-1998 W62829; W62829 standard; Protein; 666 AA (RETR-) COOP Goulter KC, RES CENT TROPICAL PLANT PATHOLOGY (first entry) 96AU-0004275 97WO-AU00874 /note= "signal peptide"
29..666 Location/Qualifiers /note= "mature protein" Green JL, Manners JM, Marcus JP;

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RESULT
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Query Match
Best Local Similarity 96.1
Matches 640; Conservative
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                                       \verb|hiakflqtistpggykeffpaggqnpepylstfskeileaalntqteklrgvfgqqregv|\\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 34-36;
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                                                                    Query Match
Best Local S
Matches 604
                                                                                                                                                                                    be used animals.
                                                                                                                                                                                                The sequence is that of an antimicrobial protein whibe used to control microbial infestations in plants
                                                                                                                                                                                                                                                                              Novel anti-microbial protein from e.g. Macadamia integrifolia -useful for controlling microbial infestations of plants or mammals \ensuremath{\mathsf{u}}
                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                    Claim
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Recombinant cocoa proteins - are responsible for flavour in cocoa beans and produced in large quantities using yeast and bacterial
                                                 WPI; 1992-024418/03.
N-PSDB; Q20377.
                                                                                                                                                                                                                                                                                                                                                       Sequence encoded by 67 kD T.
                                                                                                  Spencer
                                                                                                                                                                 11-JUN-1990;
                                                                                                                                                                                                 07-JUN-1991;
                                                                                                                                                                                                                                                                                                                               Cocoa; flavour; vicilin; seed storage
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Best Local
           antimicrobial
                                 Gossypium hirsutum antimicrobial protein
                                                                            W62832
                                                                                                 W62832 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The inventors claim a 67 kD and 31 kD T. cacao protein, and fragments, and encoding DNAs. The 47 kD and 31 kD proteins are derived from the 67 kD precursor. T. cacao protein cDNA was detected in a cDNA library prepared from immature cocoa beans RNA using a probe based on the AA sequence of a CNBr peptide common to the 47 kD and 31 kD polypeptides. Homology searches revealed close homologies between the 67 kD polypeptide and the vicilins, which are
                                                      27-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                   ifnnpdesyfmsfsqqrqr---rderrgnplasildf
                                                                                                                                                                                                                                                                                                                                                                                                                   ICEEEEEYNR---QRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRY 165
                                                                                                                                                                           LFNSQDESIFFPGPRQHQQQSSRSTKQQQPLVSILDF 663
                                                                                                                                                                                                             GHPVVFVSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEE
                                                                                                                                                                                                                                                                                                  YNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVV
                                                                                                                                                                                                                                                                                                                                                                          vpagstvyvvsqdnqekltiavlalpvnspgkyelffpagnnkpesyygafsyevletvf\\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEQQREDEEKYEERMKEEDNKRDPQQREYEDCRRRCEQQE--PRQQYQCQRRCREQQRQH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          storage proteins.
                                                                                                                                                                                               ghavtffaskdqplnavafglnaqnnqriflagk-knlvrqmdseakelsfgvpsklvdn
                                                                                                                                                                                                                                           tdgygyaqmacphlsrqsqgsqsgrqdrreqeeeseeetfgefqqvkaplspgdvfvapa
                                                                                                                                                                                                                                                                  ASGEADVEMACPHLSGRHGGRRGGK--RHEEEEDV-----HYEQVKARLSKREAIVVPV
                                                                                                                                                                                                                                                                                      inllsqspvysnqngrffeacpedfsqfqnmdvavsafklnqgaifvphynskatfvvfv
                                                                                                                                                                                                                                                                                                                                ntqrekleeileeqrggkrqqgqgmfrkakpeqiraisqqatspr----hrgge--rla
                                                                                                                                                                                                                                                                                                                                                      NTQAERLRGVLGQQR-----EGVIISASQEQIRELTRDDSESRRWHIRRGGESSRGP
                                                                                                                                                                                                                                                                                                                                                                                                IPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRGGDLINPQRGGSGRYEEGEEKQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        keqqrqqeeel-----qrqyqqcqgrcqeqqqqqreqqqcqrkcweqykeq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lcsgvsaygrkqyerdprqqyeqcqrrceseateereqeqceqrcer-----ey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 107; Mismatches 175;
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; 59pp;
           protein;
                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.4%; Score 1145; DB 13; 41.1%; Pred. No. 1.4e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
           infestation; control
                                                                                                  590
                                                                                                                                                                                                                                                      <del>--</del>
                                                                                                                                                      562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be used animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-377279/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gossypium hirsutum.
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                      525
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                                                                                                                                                                                                                                                                                                                                                                          r--qqeerqqpqcqqrclkrfeqeqqq-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 49-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goulter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     590 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96AU-0004275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-AU00874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green JL,
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The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and man
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glynqninpdhnqrifvagkinhv-rqwdsqakelafgvssrlvdeifnsnpqesyfvs-
                               G----INAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEELFNSQDESIFFPGP
                                                                                                        YRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRHGGRRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLLNRDNNERLHIAKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eqshnpfhfhrrs fqsrfree hgnfrvlqrfasrhpilrgine frlsilean pntfvlph\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRHETEPRHMOTCOQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKRDPOQRE 193
                                                                                                                                                              KRHEEEEDV-------HYEQVKARLSKREAIVVPVGHPVVFVSSGNENLLLFAF 585
                                                                                                                                                                                                               frqlrdinvtvsalqlnqgsifvphynskatfvilvtegngyaemvsphlp----rqss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hcdaekiylvtngrgtltflthenkesynivpgvvvkvpagstvylanqdnkekliiavl 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ddppkryedcrrrcewdtrgqkegqqceescksqygekdqqqrhrpedpqrryeecqqec 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDPQTDCQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR--DPQQQYEQCQERC 133
                                                                                                                                                                                                                                                                                                                          {\tt gmfrkasqeqiralsqeatspr----eksge--rfafnllsqtprysnqngrffeacppe}
                                                                                                                                                                                                                                                                                                                                                                                GVIISASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPED 478
                                                                                                                                                                                                                                                                                                                                                                                                                                   hr pvnnpg qf eeff pags qrpq sylrafs reile pafntr seql delf ggrqsrrrqq gq\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fqecqqhchqqeqrpekkqqcvrecrekyqe----npwrgereeeaeeeeteegeq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 31.3%; Score 1105.5; al Similarity 38.4%; Pred. No. 5.5% 233; Conservative 113; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 5.5e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Manners JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o; DB 19; Length .5e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marcus
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W62831
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      Matches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 47-49; 96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-377279/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9827805-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antimicrobial protein; infestation; control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W62831 standard;
                                                                                  176
                                                                                                                                                          283 LRALKNYRLYLLEANDNAFYLPTHLDADAILLYTGGRGALKMIHRDNRESYNLECGDVIR 342
                                                                                                                                                                                                                                                                                 166 EEQQREDEEKYEERMKEEDNKRDPQQREYEDCRRRCEQQE--PRQQYQCQRRCREQQRQH 223
                                                                                                                                                                                                                                                                                                                                         109 ICEEEEEEYNR----QRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRY 165
455 YNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVV 514
                                                                                                                                                                                                                                                              71 keqqrqqeeel------qrqyqqcqgrcqeqqqqqqreqqqcqrkcweqykeq 116
                                                                                                                                                                                                                                                                                                                       22 lcsgvsaygrkqyerdprqqyeqcqrrceseateereqeqceqrcer-----ey 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                                                                                     GRGGDLINPQRGGSGRYEEGEEKQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKL 282
                                              NTQAERLRGVLGQQR------EGVIISASQEQIRELTRDDSESRRWHIRRGGESSRGP 454
                                                                                                                IPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAAL 402
                                                                                                                                                                                                       er-gehenyhnhkknrseeeegggrnnpyyfpkrrsfgtrfrdeegnfkilgrfaenspp
                           ntqrekleeileeqrgqkrqqgqqgmfrkakpeqiralsqqatspr----hrgge--rla
                                                                                                                                             {\tt lkgindyrlamfeanpntfilphhcdaea} iy fvtngkgtit fvthenkes ynvqrgtvvs
                                                                                                                                                                                                                                                                                                                                                                                                                                                              525 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    29.3%; Score 1036; DB 19;
41.4%; Pred. No. 8.3e-85;
ative 91; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Green JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manners JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marcus
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 525;
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W62835
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Best Local Similarity
Matches 201; Conserv
                                                                                                                                                                                                                                                                                                                   The sequence is that of an antimicrobial protein which \boldsymbol{\alpha} be used to control microbial infestations in plants and animals.
                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 58-60; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Novel anti-microbial protein from e.g. Macadamia useful for controlling microbial infestations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antimicrobial protein; infestation;
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-377279/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bower NI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W62835 standard; Protein; 593 AA
                                    351 LINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLR 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-OCT-1998 (first entry)
411 GVLGQ -- QREGVIISASQEQIRELTRDDSE---- SRRWHIRRGGESSRGPYNLFNKRPLYS
                           200
                                                                                       236
                                                                                                                                                                                          182 EEDNKRDPQQREYEDCRRRCEQQEPRQQYQCQRRCRE-----QQRQHGRGGDLINPQRG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350
                                                                                                                            90
                                                                                                                                                                         25 eddnhhhhgghksgqcvrrcedrpwhqrprcleqcreeerekrqersrheadd----rs 79
                   lantdgrkklvitkilhtisvpgefqfffgpggrnpesflssfsksiqraayktssdrle
                                                                                                                                         | GSG----RYEEGEEKQSD-NPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYR 290
                                                                       gegssederegekekgkdrrpyvfdrrsfrrvvrseggslrvlrpfdevsrllrgirdyr 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GHPVVFVSSGNENLLLFAFGINAQNNHENFLAGR 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ghavtffaskdqplnavafglnaqnnqriflagr 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tdgygyaqmacphlsrqsqgsqsgrqdrreqeeeseeetfgefqqvkaplspgdvfvapa 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASGEADVEMACPHLSGRHGGRRGGK--RHEEEEEDV------HYEQVKARLSKREAIVVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goulter KC,
                                                                                                                                                                                                                                                                                              593
                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-AU00874
                                                                                                                                                                                                                           25.3%; Score 895; DB 39.6%; Pred. No. 4.9e tive 83; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Green JL, Manners JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           control.
                                                                                                                                                                                                                                         DB 19;
.9e-72;
                                                                                                                                                                                                                               183;
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                                                                                                                                                                                                                                                    Length 593;
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                                                                                                                                                                                               Matches
                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                    The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 60-62; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel anti-microbial protein from e.g. Macadamia useful for controlling microbial infestations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9827805-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antimicrobial protein; infestation; control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W62837 standard; Protein; 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-377279/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hordeum vulgare antimicrobial protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bower NI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hordeum vulgare
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                                                                                                                                                       SKYDNQDDPQ--TDCQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQRDPQQQYE 127
                                                                          QCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEE-----KYEERMKE 182
                                                                                                                ashddeddrrgghslqqcvqrcrqer--pr---ysharcvqec-----rddqqqh- 71
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                                                                                                                                                                                                                                                                                               637 AA;
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                                                                                                                                                                                                                   24.8%; Score 875; DB 19; Length 637; 35.6%; Pred. No. 3.5e-70;
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                                                                                                                                                                                                 99; Mismatches 206;
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                  Bannon GA,
                                                                                            04-MAR-1996;
29-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                          Key
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                                                                                                                                                         23-SEP-1996;
                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peanut allergen Ara hI.
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                                                      (UYAR-) UNIV ARKANSAS
                                                                                                                                                                                             10-JUL-1997.
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| eergrg-----hgrhgege-----reeergrgrgrhgegerceeegrgrg
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                  Burks AW,
                                                                                          96US-0610424
95US-0009455
                                                                                                                                                         96WO-US15222
                                                                                                                                                                                                                                                                                               /label= Mat_protein
521..523
                                                                                                                                                                                                                                                                                                                                  /label= Sig_peptide 23..614
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                Cockrell G,
                                                                                                                                                                                                                                                                       "N-glycosylation site"
                  Helm RM,
                Stanley JS;
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459 525 399 465

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414

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           FSKEILEAALNTQAERLRGVL-------GQQR------EGVIISASQEQIREL
                                                                                         YNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLST
                                                                                                                                       shqqprkirpegrege----qewgtpgsevreetsrnnpfyfpsrrfstrygnqngrirv
                                                                                                                                                                                                     REQQ-----RQHGRGGDLINPQRGGSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISV 272
                                                                                                                                                                                                                                                             KQQKRYEEQQREDEEKYEERMKEEDNK----RDPQQREYEDCRRRCEQQEPRQQYQCQRRC 216
tkhaksvs----kkgseeeditnpinlrdgepdlsnnfgrlfevkpdkknpqlqdldmml
                                                                                                                                                                LENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHLDADAILLVTGGRGALKMIHRDNRES
                                                                                                                                                                                                                                     rqpgdydddrrqpr-----reeggrwgpaeprereree----dwrqpredw---rrp 133
                                           fsrntleaafnaefneirrvlleenaggeqeergqrrrstrssdnegvivkvskehvqel
                                                                                                                                                                                                                                                                                                                                      208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypogaea antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goulter KC,
                                                                                                                                                                                                                                                                                                                                                                                               614 AA;
                                                                                                                                                                                                                                                                                                                                   24.7%; Score 873.5; DB 19; ilarity 34.3%; Pred. No. 4.5e-70; Conservative 115; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96AU-0004275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-AU00874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Green JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Manners JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       integrifolia
plants or man
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                mammalian
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                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                    432
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RESULT
Y15244
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Query Match
Best Local S
Matches 213
                                                                                                                                                                                                                                                                                                                  13-FEB-1998;
13-FEB-1998;
13-FEB-1998;
                                                                      By modifying the IgE binding sites the ability of the allergen to provoke an immune response is downregulated. The epitopes of the IgE binding sites can therefore be modified in genetically engineered plants and animals to elicit less of an allergic response.
                                                                                                                  epitopes,
Y15263).
                                                                                                                         This is the amino acid sequence of the Ara h 1 protein from Arachis hypogea. The Ara h 1 protein has 23 IgE (Immunoglobulin E) binding epitopes, four of which are immunodominant (Y15247, Y15249, Y15250)
                                                                                                                                                                                        \begin{array}{ll} \textbf{Modified allergen with reduced IgE} \\ \textbf{allergies} \end{array}
                                                                                                                                                                                                                                                                        (SOSI/) SOSIN H.
(UYAR-) UNIV ARKANSAS.
(UYNY) UNIV NEW YORK
                                                     Sequence
                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                 27-AUG-1998;
31-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                     05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                        W09938978-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           Arachis hypogea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peanut allergen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y15244 standard;
                                                                                                                                                                                                                                                                                                                                                                                29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin
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nes 213; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIANITQGSMMGPFFNTRSTKVVVVVASGEADVEMACPIILSGRHGGRRGGKRHEEEEEDVHY
                                                                                                                                                                                                                                                       GA,
                                                                                                                                                                                                                        Z06382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune
                                                     626
                                                                                                                                                                    Page 35-37;
                                                                                                                                                                                                                                                      Burks AW,
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                 98US-0141220.
98US-0073283.
98US-0074590.
98US-0074624.
98US-0074633.
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                                                     AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ara h 1, amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ιg
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                                                                                                                                                                  46pp;
                                                                                                                                                                                                                                                      Sampson
                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding
                                                                                                                                                                                                                                                                         SINAI SCHOOL MEDICINE
  105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           626
 Score 865.5;
Pred. No. 2.4e
D5; Mismatches
                                                                                                                                                                   English.
                                                                                                                                                                                                                                                      HA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               site;
                                                                                                                                                                                                  binding,
                                                                                                                                                                                                                                                       Sosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               peanut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergen; epitope;
  es 209;
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                     DB 20;
                                                                                                                                                                                                  useful for treating
  Indels
                    Length
                      626;
  87;
Gaps
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**T** i

21-SEP-1998; 09-JAN-1998;

98GB-0020474 98GB-0000445

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RESULT 12
Y25657
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                                                                                                                                                                                                                                                                                                                Major histocompatibility complex; class II; desensitising; human; allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting; chiromidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee; screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat; cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
                                                                           11-JAN-1999;
                                                                                                                                                                                                                                  Arachis hypogea
                                                                                                                                                                                                                                                                                               mice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peanut allergen 1168391 Ara h I protein fragment.
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                                                                                                                                                                                                                                                                                          treatment; prevention; hypersensitivity;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptiderived from the allergen where restriction to a MHC Class I molecule possessed by the patient can be demonstrated for the peptide and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                         HLSGRHGGRRGGKRHEEEEDV----HYEQVKARLSKREAIVVPVGHPVVEVSSGNENLLL 582
                                                                                                                                                                                            fgklfevkpdkknpqlqdldmmltcveikegalmlphfnskamvivvvnkgtgnlelvav
                                                                                                                                                                                                                                                        YGQAYEVKPEDYR-QLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQTISTP 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgttnqrsppgertrgrqpgdydddrr--qprreeggrwgpagprerereed-wrqpr-- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MQTCQQRC---ERR----YEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKRDPQQR 192
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Pred. No. 2.4e-
05; Mismatches
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nes 209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 626;
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Ъ Qy DЬ Qy Вb Q В Q DЬ

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Matches 212; Best Local Similarity

Conservative

105;

Mismatches

210;

Indels Length

87;

Gaps

18;

24.3%;

Score 859.5; DB 1 Pred. No. 8.4e-69;

DB 18;

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                                                        This polypeptide comprises major peanut allergen Ara hI (W22149). Its sequence was deduced from cDNA clone P41b (T76613), isolated from peanut seed cDNA using a primer (see T76616) based on an isolated Ara hI peptide (see W24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The allergen is recognised by serum IgE from a large proportion of individuals with peanut hypersensitivity. Ara hI and Ara hII (see W24164) can be used to raise monoclonal antibodies which are used in a specific two-site was the second of the detection of Ara hII or Ara hII (claimed). IgE-
Sequence
                      e.g. anaphylactic shock.
                                 binding Ara hI antigen epitopes (see W24165-87) may be used vaccines to protect against allergic reactions to peanut all
                                                                                                                                                                                                     Claim 31; Page 172; 354pp; English.
                                                                                                                                                                                                                                                                                                                                                               04-MAR-1996;
29-DEC-1995;
                                                                                                                                                                                                                                Peanut allergens Ara hI and Ara hII - used for vaccination and in two-site monoclonal antibody based {\tt ELISA}
                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                            Bannon GA,
                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monoclonal antibody; ELISA; analysis; Ara hI.
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                                                                                                                                                                                                                                                                       T76613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anaphylactic
626 AA;
                                                                                                                                                                                                                                                                                                            Burks AW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   storage protein; allergen; allergy; hypersensitivity;
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95US-0009455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Sig_peptide
23..626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=_Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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RESULT 14
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           WPI; 1998-377279/32
                                  Bower NI,
                                                                                  20-DEC-1996;
                                                                                                        22-DEC-1997;
                                                                                                                                02-JUL-1998
                                                                                                                                                       WO9827805-A1
                                                                                                                                                                                Glycine max
                                                                                                                                                                                                       antimicrobial
                                                                                                                                                                                                                             Glycine max antimicrobial protein.
                                                                                                                                                                                                                                                      27-OCT-1998
                                                                                                                                                                                                                                                                                                   W62838 standard; Protein; 605 AA.
                                                          (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HQQQSSRSTKQQQP 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----EGVIISASQEQIRELTRDDSESRRWHIRRGGESSRG----PYNLFNKRPLYSNK 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVL------GQQR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --edwrrpshqq-pr-----kirpegrege----gewgtpgshvreetsrnnpf 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sqsqspsspekesp 602
                                                                                                                                                                                                                                                                                                                                                                                                         -gfginaennhriflagdkdnvidgiekqakdlafpgsgeqvekliknqkeshfvsarpg 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGQAYEVKPEDYR-QLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACP 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgttnqrsppgertrgrqpgdydddrr--qprreeggrwgpagprerereed-wrqpr-- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLSGRHGGRRGGKRHEEEEDV----HYEQVKARLSKREAIVVPVGHPVVFVSSGNENLLL 582
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                                  Goulter KC,
                                                                                                                                                                                                                                                     (first entry
                                                                                                                                                                                                       protein; infestation; control.
                                                                                  96AU-0004275
                                                                                                        97WO-AU00874.
                                  Green
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                                  Manners JM,
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RESULT 15 Y40999

Y40999 standard; protein; 605

AΑ

06-DEC-1999 (first entry)

Peanut; allergen; Ara H 1; IgE; immunoglobulin E; epitope; allergic reaction; soybean; beta-conglycinin.

Ara h 3;

Soybean beta-conglycinin protein sequence.

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of an antimicrobial protein which obe used to control microbial infestations in plants and
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eegnkgrk--gplssil 601
                  QQSSRSTKQQQPLVSIL 661
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                                                                                           FGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEELFNSQDESIFFPGPRQHQ
                                                                                                                          -----glkeqqqeeqqlevrkyraelseqdifvipagypvvv--natsnlnffa
                                                                                                                                                          HLSGRHGG--RRGGKRHEEEEDVHYEQVKARLSKREAIVVPVGHPVVFVSSGNENLLLFA 584
                                                                                                                                                                                           klgkffeitpeknpqlrdldiflsivdmnegalllphfnskaivilvinegdanielv--
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                                                                                                                                                                                                                                                                                      -----GQQR--EGVIISASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSN 466
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                                                                                                                                                                                                                                                                                                                                     ERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ywekenpkhn--kclqscnserdsyrnqa-charcnllkvekeeceegeiprprprpqhp 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 63-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides a tertiary structure for the peanut allergen Ara H 1. The Ara H 1 allergen is found to contain 23 linear IgE-binding epitopes. The invention also provides an isolated recombinant peanut allergen designated Ara h 3 and a nucleotide molecule encoding the peanut allergen Ara h 3. Molecules of the invention are used to protect a host animal from allergic reaction, particularly using a modified allergen which is less reactive with IgE. The invention may also be used to ensure that the allergen is not introduced into genetically modified food. The present sequence represents a soybean beta-conglycinin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tertiary structure of peanut allergen \mbox{\rm Ara } h \ 1 for protection of a host animal from allergic reaction -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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ivsnklgkffeitpeknpqlrdldiflsivdmnegalllphfnskaivilvinegdanie
                                                                                                                                                                                                                 LEANPNAFVLFTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIFAGTTFYLIN 353
                                                                                                                                                                                                                                                                                  ------GQOR--EGVIISASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRP 462
                                                                                                                                                                 RDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVL 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                  RDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEER 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                wekknpkhn-----kclqscnserdsyrnga-charcnllkvekeeckkgeiprprprp
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99US-0077763.
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